AMENDMENTS TO THE CLAIMS

1.   (Currently Amended) A sample analyzing method, which comprises:

(a) adding at least one reference material to each of multiple samples;

(b) obtaining three-dimensional data as a result of liquid chromatography mass spectrometry for the multiple samples, wherein the three-dimensional data comprises a parameter indicating a mass-to-charge ratio, a parameter indicating ionic intensity, and a parameter indicating a retention time;

(c) correcting the parameter indicating a retention time in the three-dimensional data for the multiple samples using at least one peak of the at least one reference material;

(d) comparing the corrected data obtained in said step (c) for the multiple samples to analyze differences among the multiple samples; and

(e) outputting a result of the comparison in step (d).

2.   (Canceled)

3.   (Previously Presented) The sample analyzing method according to claim 1, wherein, in said step (c), profiles regarding parameters, from which a parameter as a correction target has been excluded, are used as reference profiles, and wherein using an evaluation function acting as a scale of position similarity regarding a plurality of reference profiles among multiple samples, the position of each profile is determined as a problem of finding an optimum solution which optimizes the value of said evaluation function.

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4.   (Original) The sample analyzing method according to claim 3, wherein said

evaluation function is defined with one or more terms selected from the group consisting of the

following terms (1) to (5):

(1) a term regarding similarity and/or distance among profiles regarding a parameter of a

correction target;

(2) a term regarding similarity and/or distance among profiles regarding a reference

profile;

(3) a term regarding the degree of concordance of data points among profiles as

comparison targets;

(4) a term regarding the degree of discordance of data points among profiles as

comparison targets;

(5) a term regarding the degree of concordance or discordance of reference material-

derived signals among profiles as comparison targets; and

(6) a term regarding the degree of concordance in the previous comparison during

repeated comparison operations.

5.   (Previously Presented) The sample analyzing method according to claim 3,

wherein, in said step(c), dynamic programming algorithm is used, when the value of said

evaluation function is optimized as a problem of finding an optimum solution regarding said

parameter of a correction target.

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6.   (Original) The sample analyzing method according to claim 5, wherein, in said

dynamic programming algorithm, when the optimal correspondence of data points contained in a

parameter of a correction target is evaluated by calculating scores, the score of a correspondence

regarding data points derived from a reference material is set by a point-addition scoring system.

7.   (Original) The sample analyzing method according to claim 5, wherein, in said

dynamic programming algorithm, when the optimal correspondence of data points contained in a

parameter of a correction target is evaluated by calculating scores, a constraint condition is set, in

which a correspondence regarding data points derived from a reference material is necessarily

corresponded at a designated point.

8.   (Previously Presented) The sample analyzing method according to claim 1,

wherein said multiple samples comprise a protein group and/or a peptide group.

9.   (Cancelled)

10.   (Previously Presented) The sample analyzing method according to claim 1,

wherein said at least one reference material is at least one type of peptide selected from the group

consisting of peptide T (Ala-Ser-Thr-Thr-Asn-Tyr-Thr)(**SEQ ID NO: 1**), β-casomorphin-7 (Tyr-

Pro-Phe-Pro-Gly-Pro-Ile)(**SEQ ID NO: 2**), and a structural analog thereof.

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11.   (Previously Presented) The sample analyzing method according to claim 1,

wherein each of said at least one reference material is added to said multiple samples in a state

where it is immobilized in gel.

12.   (Currently Amended) A computer-readable medium on which is embodied a

sample analyzing program comprising instructions which, when executed, cause a computer to

execute:

a procedure (a) of inputting three-dimensional data obtained as a result of liquid

chromatography mass spectrometry for multiple samples to each of which at least one reference

material has been added, wherein the three-dimensional data comprises a parameter indicating a

mass-to-charge ratio, a parameter indicating ionic intensity, and a parameter indicating a

retention time;

a procedure (b) of correcting the parameter indicating a retention time in the three-

dimensional data for the multiple samples using at least one peak of the reference material; and

a procedure (c) of comparing the data corrected in said procedure (b) for the multiple

samples to analyze differences among the multiple samples; and

a procedure (d) of outputting a result of the comparison in said procedure (c).

13.   (Cancelled)

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14.   (Previously Presented) The computer-readable medium according to claim 12,

wherein, in said procedure (b), profiles regarding parameters, from which a parameter as a

correction target has been excluded, are used as reference profiles, and wherein using an

evaluation function acting as a scale of position similarity regarding a plurality of reference

profiles among multiple samples, the position of each profile is determined by optimizing the

value of said evaluation function as a problem of finding an optimum solution.

15.   (Previously Presented) The computer-readable medium according to claim 14,

wherein said evaluation function is defined with one or more terms selected from the group

consisting of the following terms (1) to (5):

(1) a term regarding similarity and/or distance among profiles regarding a parameter of a

correction target;

(2) a term regarding similarity and/or distance among profiles regarding a reference

profile;

(3) a term regarding the degree of concordance of data points among profiles as

comparison targets;

(4) a term regarding the degree of discordance of data points among profiles as

comparison targets;

(5) a term regarding the degree of concordance or discordance of reference material-

derived signals among profiles as comparison targets; and

(6) a term regarding the degree of concordance in the previous comparison during

repeated comparison operations.

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16.   (Previously Presented) The computer-readable medium according to claim 14, wherein, in said procedure (a), dynamic programming algorithm is used, when the value of said evaluation function is optimized as a problem of finding an optimum solution regarding said parameter of a correction target.

17.   (Previously Presented) The computer-readable medium according to claim 16, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, the score of a correspondence regarding data points derived from a reference material is set by a point-addition scoring system.

18.   (Previously Presented) The computer-readable medium according to claim 16, wherein, in said dynamic programming algorithm, when the optimal correspondence of data points contained in a parameter of a correction target is evaluated by calculating scores, a constraint condition is set, in which a correspondence regarding data points derived from a reference material is necessarily corresponded at a designated point.

19.   (Previously Presented) The computer-readable medium according to claim 12, wherein said multiple samples comprise a protein group and/or a peptide group, and wherein multi-dimensional data derived from said protein group and/or peptide group are analyzed.

20.   (Cancelled)

21.   (Previously Presented) The computer-readable medium according to claim 12, wherein said at least one reference material is at least one type of peptide selected from the group consisting of peptide T (Ala-Ser-Thr-Thr-Asn-Tyr-Thr)**(SEQ ID NO: 1)**, β-casomorphin-7 (Tyr-Pro-Phe-Pro-Gly-Pro-Ile)**(SEQ ID NO: 2)**, and a structural analog thereof.

22.   (Previously Presented) The computer-readable medium according to claim 12, wherein each of said at least one reference material is added to said multiple samples in a state where it is immobilized in gel.

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